

WEST Search History

DATE: Wednesday, August 18, 2004

Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
		<i>DB=USPT; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L1	(e-cloac\$ or cloacae or ecloacae).ti,ab,clm.	126
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L2	(e-cloac\$ or cloacae or ecloacae).ti,ab,clm.	460
<input type="checkbox"/>	L3	L2 same (cdna or rna or mrna or dna or nucleic or nuclear or polynucleotide or nucleotide or genetic or chromosomal or chromosome or polynucleic or polynucleic or poly-nucleotide or sequence).ti,ab,clm.	55
<input type="checkbox"/>	L4	ymfc	1
<input type="checkbox"/>	L5	rlue or rlu-e	309
<input type="checkbox"/>	L6	L5 and coli	20
<input type="checkbox"/>	L7	15 and 13	0
<input type="checkbox"/>	L8	15 and 11	0
<input type="checkbox"/>	L9	(e-cloac\$ or cloacae or ecloacae) same 15	0
<input type="checkbox"/>	L10	(e-cloac\$ or cloacae or ecloacae) and 15	0
<input type="checkbox"/>	L11	(pseudouridine or pseudo-uridine) near2 (synthase or synthetase)	55
		<i>DB=USPT; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L12	US-6110723-A.did.	1
<input type="checkbox"/>	L13	US-6361965-B1.did.	1
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L14	(pseudouridine or pseudo-uridine) near2 (synthase or synthetase).ti,clm.	8

END OF SEARCH HISTORY

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Search Results - Record(s) 1 through 8 of 8 returned.

- ☐ 1. 20020115160. 27 Sep 01. 22 Aug 02. Nucleotide sequences which code for the truB gene. Farwick, Mike, et al. 435/115; 435/199 435/252.3 435/320.1 435/69.1 536/23.2 C12P013/08 C07H021/04 C12N009/22 C12P021/02 C12N001/21 C12N015/74.
- ☐ 2. 20020037516. 19 Apr 01. 28 Mar 02. Assay for identification of a test compound. Murchie, Alastair, et al. 435/6; 435/91.2 C12Q001/68 C12P019/34.
- ☐ 3. 6361965. 12 Nov 98; 26 Mar 02. YfiI pseudouridine synthase. Powell; David J.. 435/69.1; 435/320.1 435/325 435/455 536/23.1 536/23.2 536/23.7. C07H021/04 C12P021/06 C12N015/00 C12N005/00 C12N015/63.
- ☐ 4. 6312932. 24 Mar 00; 06 Nov 01. YfiI pseudouridine synthase. Powell; David J.. 435/183; 424/185.1 424/190.1 435/233 530/300 530/350. C12N009/00 C12N009/90 A61K039/02.
- ☐ 5. 6110723. 12 Nov 98; 29 Aug 00. YfiI pseudouridine synthase. Powell; David J.. 435/233; 435/183 435/252.3 435/252.33 435/320.1 536/23.1 536/23.2 536/23.7. C12N009/90 C07H021/04.
- ☐ 6. US20020115160A. New truB gene encoding polypeptide having activity of tRNA pseudouridine 55 synthase, useful in bacteria for fermentative preparation of L-amino acids, particularly L-lysine, from glucose, molasses, starch or ethanol. BATHE, B, et al. C07H021/00 C07H021/04 C07K014/34 C12N001/21 C12N009/00 C12N009/22 C12N009/88 C12N009/90 C12N015/10 C12N015/52 C12N015/63 C12N015/74 C12P013/04 C12P013/08 C12P021/02 C12Q001/68 C12R001:15 C12P013/08.
- ☐ 7. US 6110723A. New pseudouridine synthase from *Staphylococcus aureus*, useful, e.g. in vaccines, for diagnosis of infections, and for identifying antibacterial agents. POWELL, D J. A61K039/02 C07H021/04 C12N001/20 C12N009/00 C12N009/88 C12N009/90 C12N015/19 C12N015/74 C12Q001/00.
- ☐ 8. US 6361965B. New pseudouridine synthase from *Streptococcus pneumoniae*, useful, e.g. in vaccines, for diagnosis of infections, and for identifying antibacterial agents. POWELL, D J. A01N037/18 A01N061/00 C07H021/02 C07H021/04 C07K001/00 C07K016/00 C12N005/00 C12N015/00 C12N015/63 C12P021/06 G06F017/00.

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Terms	Documents
(pseudouridine or pseudo-uridine) near2 (synthase or synthetase).ti,clm.	8

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☐ 51. [5272263](#). 18 Dec 89; 21 Dec 93. DNA sequences encoding vascular cell adhesion molecules (VCAMS). Hession; Catherine A., et al. 536/23.5; 435/320.1 435/69.6 530/380. C07K013/00 C12N015/00 C12P021/06.

☐ 52. [US20020115160A](#). New [truB](#) gene encoding polypeptide having activity of tRNA pseudouridine 55 synthase, useful in bacteria for fermentative preparation of L-amino acids, particularly L-lysine, from glucose, molasses, starch or ethanol. BATHE, B, et al. C07H021/00 C07H021/04 C07K014/34 C12N001/21 C12N009/00 C12N009/22 C12N009/88 C12N009/90 C12N015/10 C12N015/52 C12N015/63 C12N015/74 C12P013/04 C12P013/08 C12P021/02 C12Q001/68 C12R001:15 C12P013/08.

☐ 53. [US 6110723A](#). New [pseudouridine synthase](#) from *Staphylococcus aureus*, useful, e.g. in vaccines, for diagnosis of infections, and for identifying antibacterial agents. POWELL, D J. A61K039/02 C07H021/04 C12N001/20 C12N009/00 C12N009/88 C12N009/90 C12N015/19 C12N015/74 C12Q001/00.

☐ 54. [US 6361965B](#). New [pseudouridine synthase](#) from *Streptococcus pneumoniae*, useful, e.g. in vaccines, for diagnosis of infections, and for identifying antibacterial agents. POWELL, D J. A01N037/18 A01N061/00 C07H021/02 C07H021/04 C07K001/00 C07K016/00 C12N005/00 C12N015/00 C12N015/63 C12P021/06 G06F017/00.

☐ 55. [DE 19817118C](#). New nucleic acid encoding human dyskerin, for diagnosis, treatment and prevention of dyskeratosis congenita and for stabilizing chromosomes. HEISS, N, et al. A61K038/17 A61K039/395 A61K048/00 C07H021/04 C07K014/195 C07K014/435 C07K016/18 C12N001/19 C12N001/21 C12N005/10 C12N015/00 C12N015/11 C12N015/63.

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Terms	Documents
(pseudouridine or pseudo-uridine) near2 (synthase or synthetase)	55

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L4: Entry 1 of 1

File: USPT

May 13, 2003

DOCUMENT-IDENTIFIER: US 6562958 B1

TITLE: Nucleic acid and amino acid sequences relating to *Acinetobacter baumannii* for for diagnostics and therapeuticsDetailed Description Paragraph Table (9):

RODA] [SP:P15035:P13409] Contig067G 11020162_c1_541 210 4336 225 74 NO-HIT
Contig067G 11125630_f1_88 211 4337 225 74 NO-HIT Contig067G 11135962_f1_152 212
4338 807 268 476 2.60E-45 sp:[LN:YMFC_ECOLI] [AC:P75966] [GN:YMFC] [OR:ESCHERICHIA
COLI] [DE:HYPOTHETICAL 24.9 KD PROTEIN IN TRMU-ICDA INTERGENIC REGION] [SP:P75966]
Contig067G 11720307_c3_826 213 4339 1026 341 1113 8 30E-113 sp:[LN:FATD_VIBAN]
[AC:P37738] [GN:FATD] [OR:VIBRIO ANGUILLARUM] [DE:FERRIC ANGUIBACTIN TRANSPORT
SYSTEM PERMEASE PROTEIN FATD] [SP:P37738] Contig067G 11739418_c3_898 214 4340 1122
373 1048 6.40E-106 sp:[LN:PHEA_PSEST] [AC:P27603] [GN:PHEA] [OR:PSEUDOMONAS
STUTZERI] [SR:,PSEUDOMONAS PERFECTOMARINA] [EC:5.4.99.5:4.2.1.51] [DE:(EC 4.2.1.51)
(PDT) (P-PROTEIN)] [SP:P27603] Contig067G 11848562_f2_258 215 4341 189 62 NO-HIT
Contig067G 1196937_c3_883 216 4342 192 63 NO-HIT Contig067G 1203137_c3_792 217 4343
969 322 752 1.50E-74 gp:[GI:g290470] [LN:ECOSOH] [AC:M73320] [GN:sohB]
[OR:Escherichia coli] [SR:Escherichia coli (sub_strain W3110, strain K-12) DNA]
[DE:E.coli sohB gene, complete CDS.] Contig067G 1210317_c2_654 218 4344 711 236 92
1.40E-05 sp:[LN:VENB_VIBVU] [AC:P74965] [GN:VENB] [OR:VIBRIO VULNIFICUS]
[EC:3.3.2.1] [DE:DIHYDROXYBENZOATE SYNTHASE)] [SP:P74965] Contig067G
12226556_f2_276 219 4345 543 180 241 2.10E-20 pir:[LN:C64858] [AC:C64858]
[PN:probable dNTP pyrophosphohydrolase b1134] [CL:mutT domain homology]
[OR:Escherichia coli] Contig067G 12298200_f1_57 220 4346 660 219 750 2.40E-74 sp:
[LN:SODF_SYNP7] [AC:P18655] [GN:SODB] [OR:SYNECHOCOCCUS SP] [SR:PCC 7942,ANACYSTIS
NIDULANS R2] [EC:1.15.1.1] [DE:SUPEROXIDE DISMUTASE [FE],] [SP:P18655] Contig067G
1230458_f1_124 221 4347 798 265 148 3.10E-13 sp:[LN:YCFC_HAEIN] [AC:P44796]
[GN:H10638] [OR:HAEMOPHILUS INFLUENZAE] [DE:HYPOTHETICAL PROTEIN H10638]
[SP:P44796] Contig067G 12787750_c1_604 222 4348 1272 423 2035 1.70E-210 gp:
[GI:g3284000] [LN:AF073769] [AC:AF073769] [PN:serine hydroxymethyltransferase]
[GN:gttA] [OR:Acinetobacter radioresistens] [DE:Acinetobacter radioresistens serine
hydroxymethyltransferase (glyA)gene, complete cds.] Contig067G 135087_f3_455 223
4349 1218 405 797 2.60E-79 sp:[LN:DACA_HAEIN] [AC:P44466] [GN:DACA:H10029]
[OR:HAEMOPHILUS INFLUENZAE] [EC:3.4.16.4] [DE:(DD- CARBOXYPEPTIDASE) (PBP- 5)]
[SP:P44466] Contig067G 1352155_f1_138 224 4350 726 241 381 3.10E-35 sp:
[LN:YIJC_ECOLI] [AC:P27307] [GN:YIJC] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 26.6
KD PROTEIN IN UDHA-TRMA INTERGENIC REGION (ORFA)] [SP:P27307] Contig067G
1359428_c3_764 225 4351 633 210 237 5.60E-20 gp:[GI:g2565360] [LN:AF025663]
[AC:AF025663] [PN:lipoprotein] [GN:vlpA] [OR:Vibrio cholerae] [DE:Vibrio cholerae
lipoprotein (vlpA) gene, complete cds.] [NT:VlpA] Contig067G 1360317_f3_438 226
4352 246 81 NO-HIT Contig067G 13672552_c1_596 227 4353 885 294 925 7.00E-93 sp:
[LN:RS2_SPIPL] [AC:P34831] [GN:RPSB] [OR:SPIRULINA PLATENSIS] [DE:30S RIBOSOMAL
PROTEIN S2] [SP:P34831] Contig067G 13756562_c1_621 228 4354 831 276 889 4.50E-89
sp:[LN:YAAA_ECOLI] [AC:P11288] [GN:YAAA] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL
29.6 KD PROTEIN IN THRC-TALB INTERGENIC REGION] [SP:P11288] Contig067G
13786577_f1_337 229 4355 246 81 98 3.00E-05 sp:[LN:YHHP_HAEIN] [AC:P44841]
[GN:H10721] [OR:HAEMOPHILUS INFLUENZAE] [DE:HYPOTHETICAL PROTEIN H10721]
[SP:P44841] Contig067G 13869027_c1_533 230 4356 906 301 821 7.30E-82 pir:

[LN:F69419] [AC:F69419] [PN:phosphate ABC transporter, ATP-binding protein (pstB) homolog] [CL:inner membrane protein malK: ATP-binding cassette homology] [OR:Archaeoglobus fulgidus] Contig067G 13875000_f1_328 231 4357 225 74 NO-HIT Contig067G 13961502_c3_907 232 4358 672 223 NO-HIT Contig067G 14297265_c1_610 233 4359 1071 356 546 1.00E-52 pir:[LN:S47741] [AC:S47741:D65150] [PN:hypothetical transcription regulator treF-kdgk intergenic region:hypothetical protein o323] [GN:yhjC] [OR:Escherichia coli] Contig067G 14304175_c1_619 234 4360 1200 399 960 1.40E-96 gp:[GI:e1420018:g4539191] [LN:SC6A5] [AC:AL049485] [PN:probable acyl-CoA dehydrogenase] [GN:SC6A5.36] [OR:Streptomyces coelicolor]

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Portner, Ginny

From: Reynolds, Deborah
Sent: Friday, October 29, 2004 2:13 PM
To: Portner, Ginny
Subject: 09/252,691

Ginny,

I am only addressing the utility, WD, and enablement. I did not really look at the 112, 2nd and art rejections.

Maintain utility as is.

Maintain WD only on the claims with %identity or fragment language.

Maintain enablement but broaden the scope slightly to allow comprising.

Deborah Reynolds
TCPS 1600
Remsen 4D21
571-272-0734

*Per D. Reynolds
1-3, 29-31, 42-44*

